~~07 614452~~
08/090002

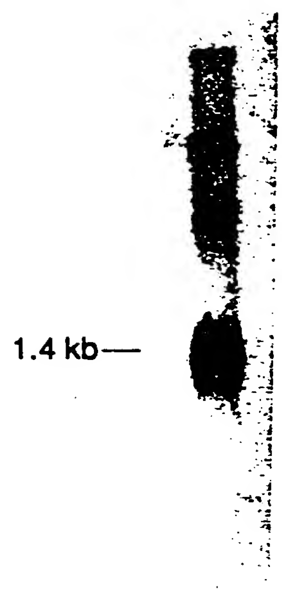

Figure 1

07/614352
08/090002

```
1     CCCTTCTCCAGGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACC   60

61    CACCTTGGGACTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCT   120

121   CCAGGACCTCAAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGG   180

181   GCTCCGCTGACTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTT   240
                                             M  L  P  V  C  H  R  F

241   TTGCGACCACCTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGC   300
       C  D  H  L  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A

301   ATCCATGGGCCCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAG   360
       S  M  G  P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S

361   CGTCCCCACACACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGTGACCC   420
       V  P  T  H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P

421   CCAGGAGGCCAGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGC   480
       Q  E  A  R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A

481   CGGAAACATTGTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGC   540
       G  N  I  V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A

541   CAGGACCTCGGGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCC   600
       R  T  S  G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P

601   CACAGAGCGCCCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGTGTGAAGATAC   660
       T  E  R  P  T  R  A  R  L  E  L  R  L  E  A  E  C  E  D  T
                                                      could be Ser

661   AGGAGGGTGGGAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCT   720
       G  G  W  E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L

721   GCTGCGCGTGCCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGT   780
       L  R  V  P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V

781   AGCCGCCAACGCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGC   840
       A  A  N  A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A

841   CACTGCAGCCTGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACG   900
       T  A  A  C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R

901   CCTGTGTCCCTTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGT   960
       L  C  P  L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V

961   GGGCACTTGTCGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTG   1020
       G  T  C  R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W

1021  GGTGATCGCGCCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGA   1080
       V  I  A  P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E

1081  AACGCTGAGGGGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCAT   1140
       T  L  R  G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M

1141  GCACGCAGCTGCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATC   1200
       H  A  A  A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S

1201  ACCCATCTCCGTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGA   1260
       P  I  S  V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D

1261  CATGGTGGTGGATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCC   1320
       M  V  V  D  E  C  G  C  R

1321  CCACGCAAAAGCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAA   1380

1381  TTTGACT   1387
```

F. 2

```
GDF-1        RRHTEPRVEVG--PVGTCRTRRLHVSF-REVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPP

Vg-1         RKRSYSKLPFT--ASNICKKRHLYVEF-KDVGWQNWVIAPQGYMANYCYGECP-YPLTEILNG--
Vgr-1        GSGSSDYNGSE--LKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGEC-SFPLNAHMNA--
BMP-2a       KRQAKHKQRKR--LKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECP-FPLADHLNS--
BMP-2b       SPKHHSQRARK--KNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCP-FPLADHLNS--
BMP-3        TLKKARRKQWI--EPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS--
DPP          -HARRPTRRKN--HDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGKCP-FPLADHFNS--
MIS          GRAQRSAGATA--ADGPCALRELSVDLRAE----RSVLIPETYQANNCQGVCGWPQSDRNPRY--
Inhibin α    RLLQRPPEEPA--AHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
Inhibin βA   GLE---CDGKV---NICC-KKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin βB   GLE---CDGRT---NLCC-RQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
TGF-β1       ALDTNYCFSST--EKNCCVRQ-LYIDFRKDLGWK-WIHEPKGYHANFCLGPCP-YIW----SLD-
TGF-β2       ALDAAYCFRNV--QDNCCLRP-LYIDFKRDLGWK-WIHEPKGYNANFCAGACP-YLW----SSD-
TGF-β3       ALDTNYCFRNL--EENCCVRP-LYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SAD-
TGF-β4       DLDTDYCFGPGTDEKNCCVRP-LYIDFRKDLQWK-WIHEPKGYMANFCMGPCP-YIW----SAD-
TGF-β5       GVGQEYCFGNN--GPNCCVKP-LYINFRKDLGWK-WIHEPKGYEANYCLGNCP-YIW----SMD-


GDF-1        ALNHAVLRALMHAAA-PTPGAGSPCCV--PERLSPISVLFF-DNSDNVVLRHYEDMVVDECGCR

Vg-1         -SNHAILQTLVHS--IEPEDIPLPCCV--PTKMSPISMLFY-DNNDNVVLRHYENMAVDECGCR
Vgr-1        -TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
BMP-2a       -TNHAIVQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-2b       -TNHAIVQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
BMP-3        --NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
DPP          -TNHAVVQTLVNN--MNPGKVPKACCV--PTQLDSVAMLYLND-QSTVVLKNYQEMTVVGCGCR
MIS          -GNH-VVLLL-KMQARGAALARPPCCV--PTAYAGKLLISLSEER--ISAHHVPNMVATECGCR
Inhibin α    -PGAPPT----PAQPYSLLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
Inhibin βA   -SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
Inhibin βB   -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
TGF-β1       -TQYSKVLALYN--QHNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF-β2       -TQHSRVLSLYN--TINPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF-β3       -TTHSTVLGLYN--TLNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS
TGF-β4       -TQYTKVLALYN--QHNPGASAAPCCV--PQTLDPLPIIYY-VGRNVRV-EQLSNMVVRACKCS
TGF-β5       -TQYSKVLSLYN--QNNPGASISPCCV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRSCNCS
```

~~07 614452~~
08/090002

Figure 3a

614452
08/090002

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF-β1	TGF-β2	TGF-β3	TGF-β4	TGF-β5
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	–	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	–	–	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	–	–	–	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	–	–	–	–	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	–	–	–	–	–	100	42	25	28	33	33	29	31	31	26	28
DPP	–	–	–	–	–	–	100	25	20	39	36	35	35	35	35	34
MIS	–	–	–	–	–	–	–	100	18	22	22	24	21	26	25	24
Inhibin α	–	–	–	–	–	–	–	–	100	23	21	24	23	24	24	24
Inhibin βA	–	–	–	–	–	–	–	–	–	100	63	38	37	36	35	38
Inhibin βB	–	–	–	–	–	–	–	–	–	–	100	35	35	36	34	32
TGF-β1	–	–	–	–	–	–	–	–	–	–	–	100	73	77	85	81
TGF-β2	–	–	–	–	–	–	–	–	–	–	–	–	100	81	68	69
TGF-β3	–	–	–	–	–	–	–	–	–	–	–	–	–	100	74	73
TGF-β4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	78
TGF-β5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100

Figure 3b

```
                                                                                  133
       54
GDF-1  PVPPVMWRLFRRRDPQEARVGRPLRPCHVEELGVAGNIVRHIPDSGLSSRPAQPARTSGLCPEWTVVFDLSNVEPTERPT
       |||   || |  |         |   | |||  | |   |  || |    |         | |    |  |  |  || |
Vg-1   PVPSILWRIFNQRMGSSIQKKKPDL CFVEEFNVPGSVIRVFPDQGRFIIPYSDDIHPTQCLEKRLFFNISAIEKEERVT
       46                                                                         124


       219            234
GDF-1  SLLLVTLDPRLCPLPR
       ||| ||| |  |  ||
Vg-1   SLLTVTLNPLRCKRPR
       228            243
```

07 ~~614452~~
08/090002

~~07 614452~~
08/090002

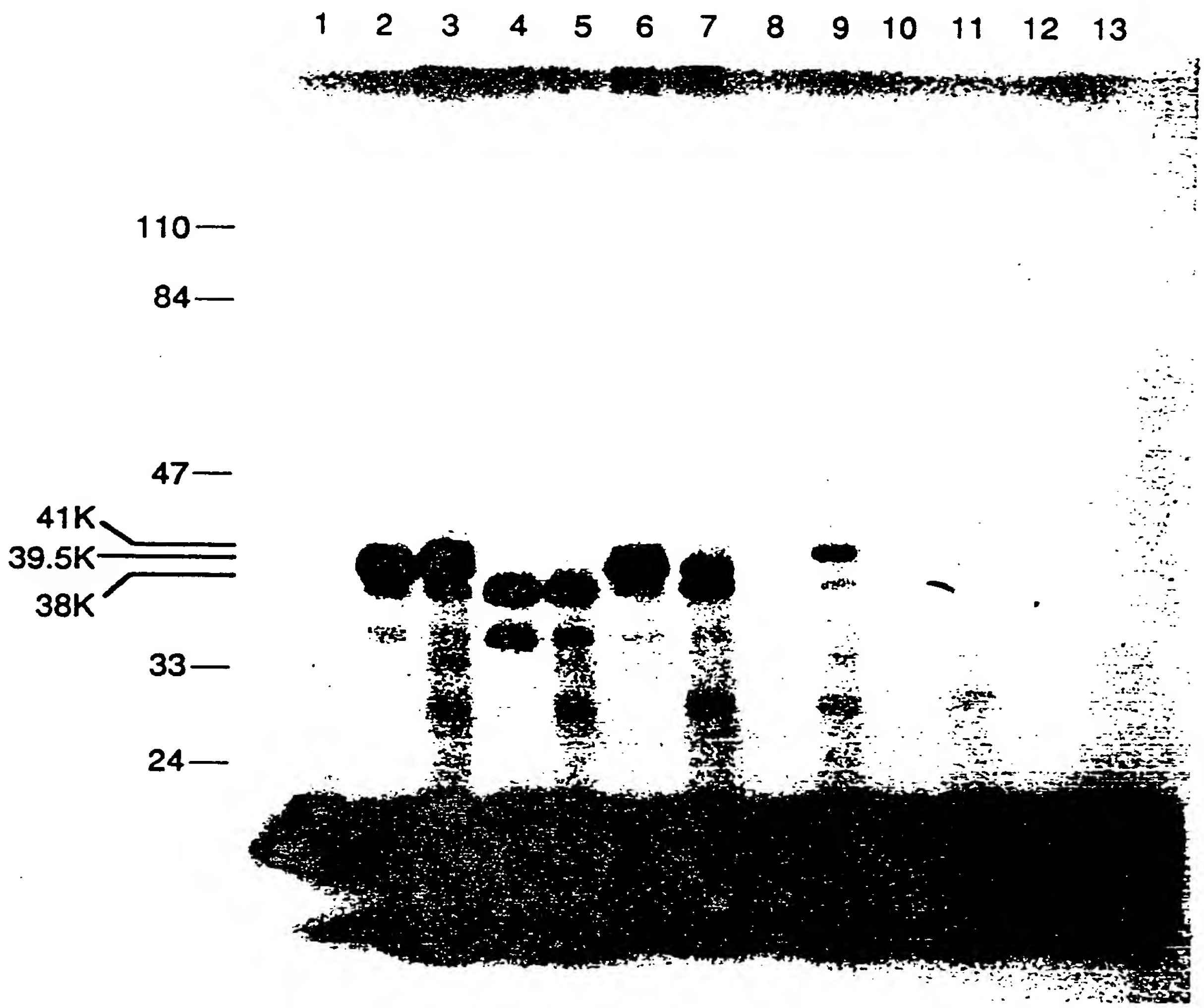

Figure 4

~~07 614452~~
08/890002

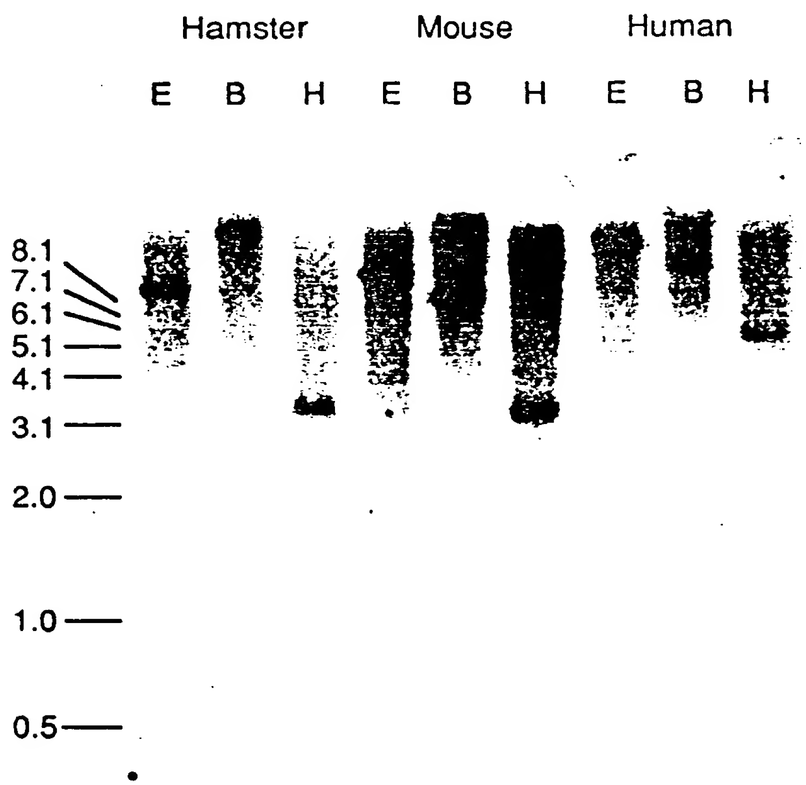

Figure 5

~~07~~ 614452
08/090002

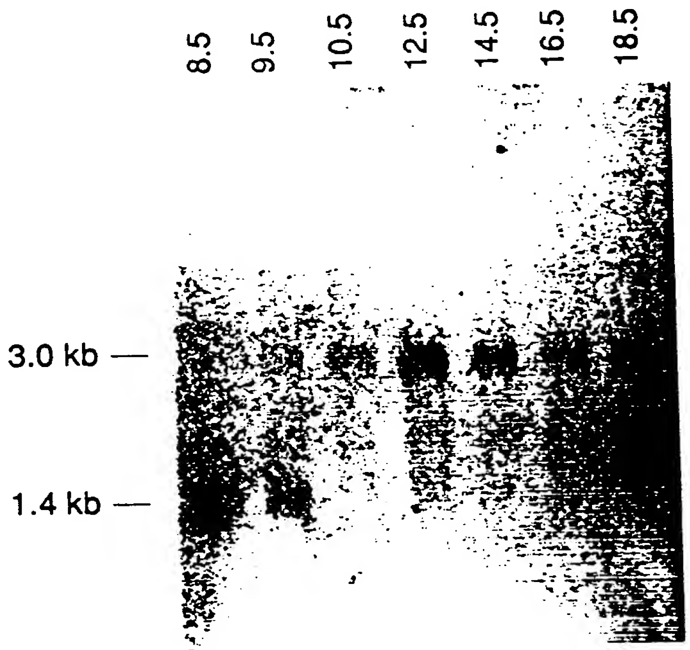

Figure 6

~~07 614452~~
08/090002

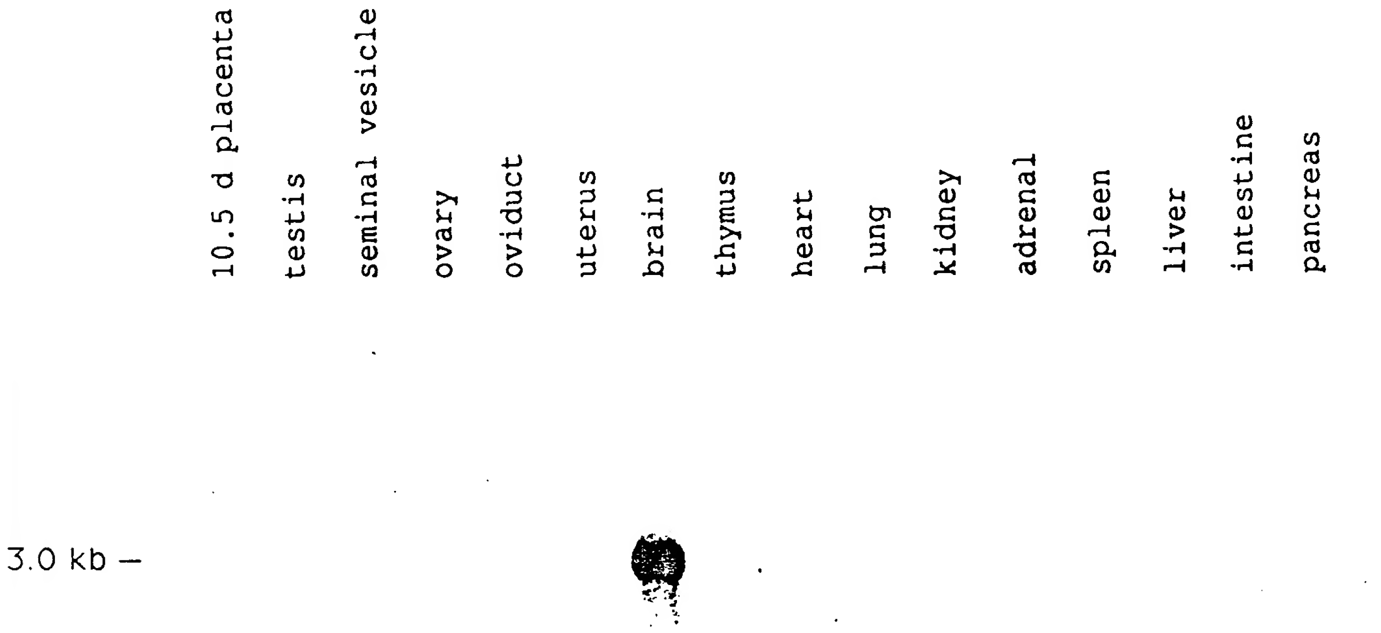

Figure 7

~~07 614452~~
06/090002

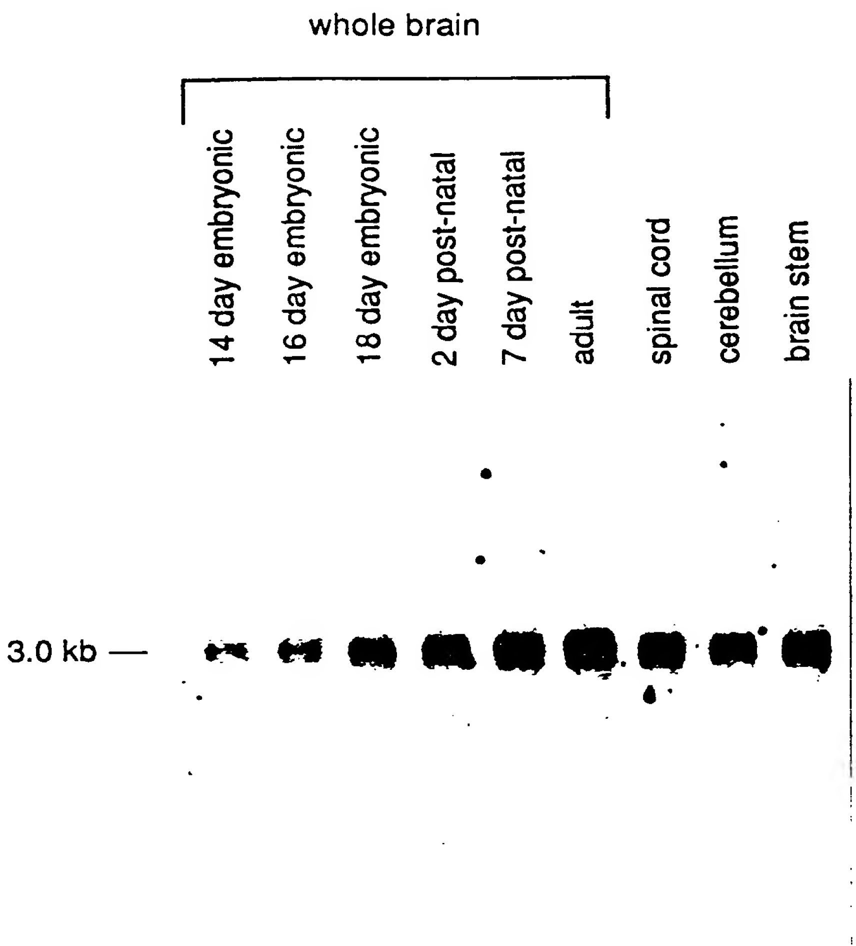

Figure 8

07 ~~614452~~
08/090002

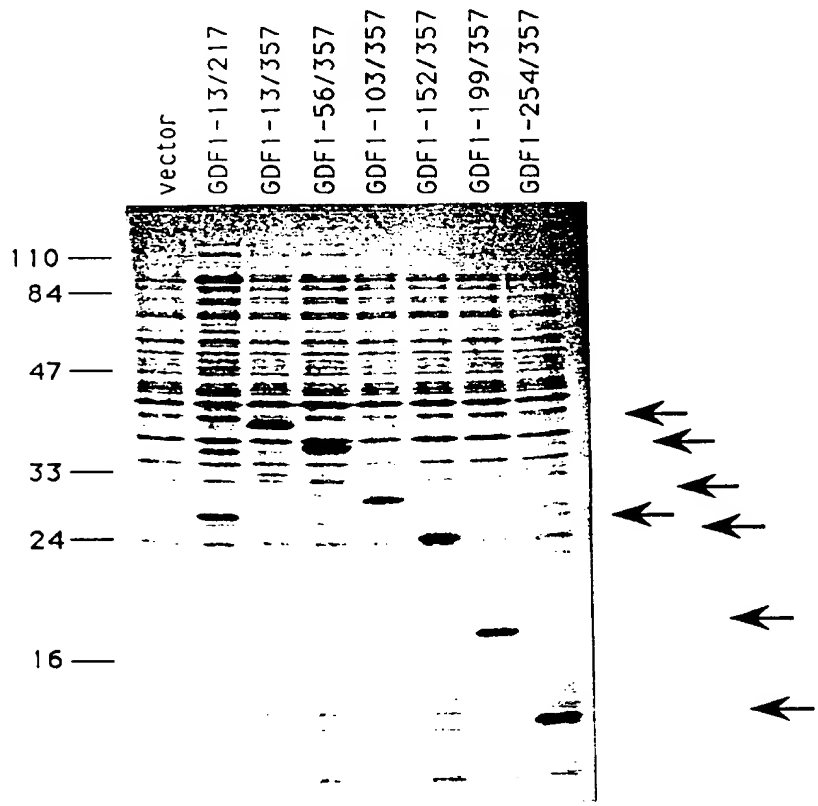

Figure 9

~~07 614452~~
P.20/26
08/090002

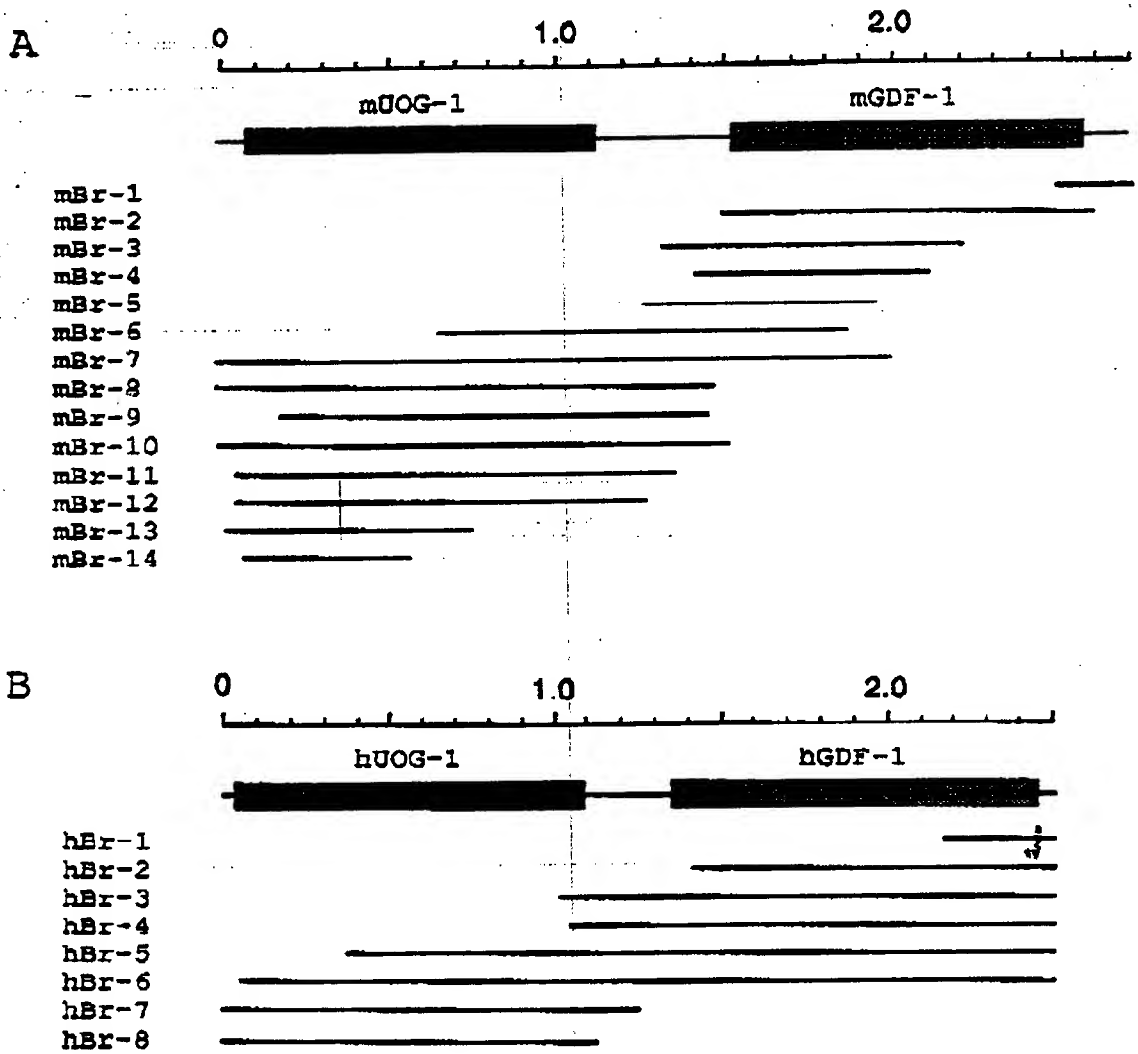

Figure 10

~~07~~ 614452
08/090002

```
1     GCGCGTGACGCGAGGGCGCGCGGCGACTCGGACCGGTGCAGGCAACAGCGGAGACAGCGG   60
61    AGAATTGGATAGCATGGCTGCTGCCGCGGCGACCCCCAGGCTCGAGGCGCCAGAGCCCAT   120
                   M  A  A  A  A  A  T  P  R  L  E  A  P  E  P  M
121   GCCGAGTTATGCGCAGATGTTGCAACGAAGCTGGGCCTCGGCGCTGGCGGCGGCTCAGGG   180
       P  S  Y  A  Q  M  L  Q  R  S  W  A  S  A  L  A  A  A  Q  G
181   CTGCGGGGACTGCGGCTGGGGACTGGCGCGCCGCGGCCTGGCGGAGCACGCGCACCTGGC   240
       C  G  D  C  G  W  G  L  A  R  R  G  L  A  E  H  A  H  L  A
241   TGCACCCGAGCTGCTGCTGGCCGTGCTCTGCGCTCTGGGGTGGACAGCGTTGCGCTGGGC   300
       A  P  E  L  L  L  A  V  L  C  A  L  G  W  T  A  L  R  W  A
301   AGCCACCACACACATCTTTCGGCCCCTGGCCAAGCGGTGTCGTCTGCAGCCTAGAGATGC   360
       A  T  T  H  I  F  R  P  L  A  K  R  C  R  L  Q  P  R  D  A
361   TGCCAGGTTACCTGAGAGCGCCTGGAAGCTTCTGTTCTACTTGGCCTGTTGGAGCTACTG   420
       A  R  L  P  E  S  A  W  K  L  L  F  Y  L  A  C  W  S  Y  C
421   CGCTTACCTGCTCCTGGGCACCAGTTATCCTTTCTTCCATGACCCGCCCTCTGTCTTCTA   480
       A  Y  L  L  L  G  T  S  Y  P  F  F  H  D  P  P  S  V  F  Y
481   TGACTGGAGGTCAGGCATGGCAGTGCCCTGGGACATCGCGGTGGCCTATTTGCTGCAGGG   540
       D  W  R  S  G  M  A  V  P  W  D  I  A  V  A  Y  L  L  Q  G
541   GAGTTTCTACTGCCACTCCATCTATGCCACCGTGTACATGGACAGCTGGCGTAAGGACTC   600
       S  F  Y  C  H  S  I  Y  A  T  V  Y  M  D  S  W  R  K  D  S
601   GGTGGTCATGCTGGTGCATCACGTGGTCACCCTGCTCCTCATTGCCTCTTCCTACGCCTT   660
       V  V  M  L  V  H  H  V  V  T  L  L  L  I  A  S  S  Y  A  F
661   CCGGTACCACAACGTAGGCCTCCTCGTGTTCTTCCTGCATGACGTCAGCGATGTGCAGCT   720
       R  Y  H  N  V  G  L  L  V  F  F  L  H  D  V  S  D  V  Q  L
721   GGAGTTCACAAAACTCAACATCTACTTTAAGGCTAGGGGTGGTGCCTACCATCGCTTGCA   780
       E  F  T  K  L  N  I  Y  F  K  A  R  G  G  A  Y  H  R  L  H
781   TGGGCTGGTGGCCAACCTGGGCTGCCTCAGCTTCTGTTTCTGCTGGTTCTGGTTCCGCCT   840
       G  L  V  A  N  L  G  C  L  S  F  C  F  C  W  F  W  F  R  L
841   CTACTGGTTCCCGCTCAAGGTTCTGTACGCCACTTGCCACTGCAGCCTGCAGTCTGTGCC   900
       Y  W  F  P  L  K  V  L  Y  A  T  C  H  C  S  L  Q  S  V  P
901   TGACATTCCGTACTACTTCTTCTTCAACATTCTGCTGTTGCTCCTGATGGTCATGAACAT   960
       D  I  P  Y  Y  F  F  F  N  I  L  L  L  L  L  M  V  M  N  I
961   CTATTGGTTCCTGTACATTGTGGCTTTCGCAGCCAAGGTGCTGACTGGTCAGATGCGTGA   1020
       Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G  Q  M  R  E
1021  ACTGGAAGACTTGAGGGAGTACGACACTCTGGAAGCTCAGACAGCCAAGCCCTGCAAAGC   1080
       L  E  D  L  R  E  Y  D  T  L  E  A  Q  T  A  K  P  C  K  A
1081  CGAGAAGCCACTGAGGAATGGCCTGGTGAAGGACAAGCTCTTCTGAGTCTCTTGTCCTCA   1140
       E  K  P  L  R  N  G  L  V  K  D  K  L  F
1141  ACTTCAGCCATCCAGGACTCTATCCCATCCTACCTGGGATACTGACTCCGCCCCTGGAGA   1200
1201  CTCGACCCAGTCCCTGGAGGTCTGCTCCCACCCCTGGAGGCCCGGTCCCGCCTTTGGCGG   1260
1261  CATGGCCTCGCCCCTAGGACAATAGCCCCGCCCTAAGATTCAGGATGCTACCCTTCTCCA   1320
1321  GGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACCCACCTTGGGA   1380
1381  CTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCTCCAGGACCTC   1440
1441  AAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGGGCTCCGCTGA   1500
1501  CTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTTTTGCGACCAC   1560
                                 M  L  P  V  C  H  R  F  C  D  H
1561  CTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGCATCCATGGGC   1620
       L  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A  S  M  G
1621  CCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAGCGTCCCCACA   1680
       P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S  V  P  T
1681  CACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGCGACCCCCAGGAGGCC   1740
       H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q  E  A
1741  AGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGCCGGAAACATT   1800
       R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A  G  N  I
1801  GTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGCCAGGACCTCG   1860
       V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A  R  T  S
1861  GGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCCCACAGAGCGC   1920
       G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P  T  E  R
1921  CCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGAGTGAAGATACAGGGGGGTGG   1980
       P  T  R  A  R  L  E  L  R  L  E  A  E  S  ~~E~~  D  T  G  G  W
1981  GAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCTGCTGCGCGTG   2040
       E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L  L  R  V
2041  CCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGTAGCCGCCAAC   2100
       P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V  A  A  N
2101  GCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGCCACTGCAGCC   2160
       A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A  T  A  A
2161  TGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACGCCTGTGTCCC   2220
       C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R  L  C  P
2221  TTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGTGGGCACTTGT   2280
       L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V  G  T  C
2281  CGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTGGGTGATCGCG   2340
       R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W  V  I  A
2341  CCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGAAACGCTGAGG   2400
       P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E  T  L  R
2401  GGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCAGCT   2460
       G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M  H  A  A
2461  GCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATCACCCATCTCC   2520
       A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S  P  I  S
2521  GTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGACATGGTGGTG   2580
       V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D  M  V  V
2581  GATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGACCGCCCCACGCAAAA   2640
       D  E  C  G  C  R
2641  GCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAATTTGACTAAA   2700
2701  AATTAAGTTCC  2711
```

Fig 11A

murine

could be cys

~~07 614452~~

08/090002

```
1     GGACACGGCGGGCGAGCGGGCGGTATGGCGGCGGCGGGGCCCGCGGCGGGGCCGACGGGG   60
                              M  A  A  A  G  P  A  A  G  P  T  G
61    CCCGAGCCCATGCCGAGCTACGCGCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG   120
      P  E  P  M  P  S  Y  A  Q  L  V  Q  R  G  W  G  S  A  L  A
121   GCGGCGCGGGGCTGCACGGACTGCGGCTGGGGGCTGGCGCGTCGCGGCCTGGCTGAGCAC   180
      A  A  R  G  C  T  D  C  G  W  G  L  A  R  R  G  L  A  E  H
181   GCGCACCTGGCGCCGCCCGAGCTGCTGCTGCTGGCGCTCGGCGCGCTGGGCTGGACCGCG   240
      A  H  L  A  P  P  E  L  L  L  L  A  L  G  A  L  G  W  T  A
241   CTGCGCTCCGCGGCCACTGCGCGCCTCTTTCGGCCCCTGGCGAAGCGGTGCTGCCTCCAG   300
      L  R  S  A  A  T  A  R  L  F  R  P  L  A  K  R  C  C  L  Q
301   CCCAGAGATGCCGCCAAGATGCCCGAGAGCGCTTGGAAGTTTCTCTTCTACCTGGGCAGC   360
      P  R  D  A  A  K  M  P  E  S  A  W  K  F  L  F  Y  L  G  S
361   TGGAGCTACAGTGCCTACCTGCTGTTTGGCACCGACTACCCCTTCTTCCATGACCCACCA   420
      W  S  Y  S  A  Y  L  L  F  G  T  D  Y  P  F  F  H  D  P  P
421   TCTGTCTTCTACGACTGGACGCCGGGCATGGCAGTGCCACGGGACATTGCAGCCGCCTAC   480
      S  V  F  Y  D  W  T  P  G  M  A  V  P  R  D  I  A  A  A  Y
481   CTGCTCCAGGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG   540
      L  L  Q  G  S  F  Y  G  H  S  I  Y  A  T  L  Y  M  D  T  W
541   CGCAAGGACTCGGTGGTCATGCTGCTCCACCACGTGGTCACTCTCATCCTCATCGTCTCC   600
      R  K  D  S  V  V  M  L  L  H  H  V  V  T  L  I  L  I  V  S
601   TCCTACGCCTTCCGGTACCACAATGTGGGCATCCTTGTGCTCTTCCTGCACGATATCAGT   660
      S  Y  A  F  R  Y  H  N  V  G  I  L  V  L  F  L  H  D  I  S
661   GACGTGCAGCTTGAGTTCACCAAGCTCAACATTTACTTCAAGTCCCGCGGCGGCTCCTAC   720
      D  V  Q  L  E  F  T  K  L  N  I  Y  F  K  S  R  G  G  S  Y
721   CATCGGCTGCATGCCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGCTTCAGCTGGTTC   780
      H  R  L  H  A  L  A  A  D  L  G  C  L  S  F  G  F  S  W  F
781   TGGTTCCGCCTCTACTGGTTCCCGCTCAAGGTCCTGTATGCCACCAGTCACTGCAGTCTG   840
      W  F  R  L  Y  W  F  P  L  K  V  L  Y  A  T  S  H  C  S  L
841   CGCACGGTGCCTGACATCCCCTTCTACTTCTTCTTCAATGCGCTCCTGCTGCTGCTCACC   900
      R  T  V  P  D  I  P  F  Y  F  F  F  N  A  L  L  L  L  L  T
901   CTTATGAACCTCTACTGGTTCCTGTACATCGTGGCGTTTGCAGCCAAGGTGTTGACAGGC   960
      L  M  N  L  Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G
961   CAGGTGCACGAGCTGAAGGACCTGCGGGAGTATGACACAGCCGAGGCCCAGAGCCTGAAG   1020
      Q  V  H  E  L  K  D  L  R  E  Y  D  T  A  E  A  Q  S  L  K
1021  CCCAGCAAAGCCGAGAAGCCACTGAGGAACGGCCTGGTGAAGGACAAGCGCTTCTGAACC   1080
      P  S  K  A  E  K  P  L  R  N  G  L  V  K  D  K  R  F
1081  CCTCGGCCCCGCCCCCGTGGACCCGGCCCCACCCCGAATACCCCGGCCACGCTCCCCGTC   1140
1141  CTTGGCCGCCCCTCCACCCCCTCCAACTCTGCTCCTCTAGGGCCGCCGCCACCTCCCCTG   1200
1201  GGACCCCGCCCCCTCATCCTGCCTCCATTTCCCGGCCACGCCCCCCAGGACCCCTGCCCC   1260
1261  TCCGGGGACACCGGCCCCGCCCTCAGCCCACTGGTCCCGGGCCGCCGCGGACCCTGCGCA   1320
1321  CTCTCTGGTCATCGCCTGGGAGGAAGATGCCACCGCCGCAGCAAGGTCCCTGCGGCCACC   1380
                                  M  P  P  P  Q  Q  G  P  C  G  H  H
1381  ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTCGCTGCCCCTGACCCGCGCCCCCGTGC   1440
        L  L  L  L  L  A  L  L  L  P  S  L  P  L  T  R  A  P  V  P
1441  CCCCAGGCCCAGCCGCCGCCCTGCTCCAGGCTCTAGGACTGCGCGATGAGCCCCAGGGTG   1500
        P  G  P  A  A  A  L  L  Q  A  L  G  L  R  D  E  P  Q  G  A
1501  CCCCCAGGCTCCGGCCGGTTCCCCCGGTCATGTGGCGCCTGTTTCGACGCCGGGACCCCC   1560
        P  R  L  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q
1561  AGGAGACCAGGTCTGGCTCGCGGCGGACGTCCCCAGGGGTCACCCTGCAACCGTGCCACG   1620
        E  T  R  S  G  S  R  R  T  S  P  G  V  T  L  Q  P  C  H  V
1621  TGGAGGAGCTGGGGGTCGCCGGAAACATCGTGCGCCACATCCCGGACCGCGGTGCGCCCA   1680
        E  E  L  G  V  A  G  N  I  V  R  H  I  P  D  R  G  A  P  T
1681  CCCGGGCCTCGGAGCCTGTCTCGGCCGCGGGGCATTGCCCTGAGTGGACAGTCGTCTTCG   1740
        R  A  S  E  P  V  S  A  A  G  H  C  P  E  W  T  V  V  F  D
1741  ACCTGTCGGCTGTGGAACCCGCTGAGCGCCCGAGCCGGGCCCGCCTGGAGCTGCGTTTCG   1800
        L  S  A  V  E  P  A  E  R  P  S  R  A  R  L  E  L  R  F  A
1801  CGGCGGCGGCGGCGGCAGCCCCGGAGGGCGGCTGGGAGCTGAGCGTGGCGCAAGCGGGCC   1860
        A  A  A  A  A  A  P  E  G  G  W  E  L  S  V  A  Q  A  G  Q
1861  AGGGCGCGGGCGCGGACCCCGGGCCGGTGCTGCTCCGCCAGTTGGTGCCCGCCCTGGGGC   1920
        G  A  G  A  D  P  G  P  V  L  L  R  Q  L  V  P  A  L  G  P
1921  CGCCAGTGCGCGCGGAGCTGCTGGGCGCCGCTTGGGCTCGCAACGCCTCATGGCCGCGCA   1980
        P  V  R  A  E  L  L  G  A  A  W  A  R  N  A  S  W  P  R  S
1981  GCCTCCGCCTGGCGCTGGCGCTACGCCCCCGGGCCCCTGCCGCCTGCGCGCGCCTGGCCG   2040
        L  R  L  A  L  A  L  R  P  R  A  P  A  A  C  A  R  L  A  E
2041  AGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCCCGGCCGC   2100
        A  S  L  L  L  V  T  L  D  P  R  L  C  H  P  L  A  R  P  R
2101  GGCGCGACGCCGAACCCGTGTTGGGCGGCGGCCCCGGGGGCGCTTGTCGCGCGCGGCGGC   2160
        R  D  A  E  P  V  L  G  G  G  P  G  G  A  C  R  A  R  R  L
2161  TGTACGTGAGCTTCCGCGAGGTGGGCTGGCACCGCTGGGTCATCGCGCCGCGCGGCTTCC   2220
        Y  V  S  F  R  E  V  G  W  H  R  W  V  I  A  P  R  G  F  L
2221  TGGCCAACTACTGCCAGGGTCAGTGCGCGCTGCCCGTCGCGCTGTCGGGGTCCGGGGGGC   2280
        A  N  Y  C  Q  G  Q  C  A  L  P  V  A  L  S  G  S  G  G  P
2281  CGCCGGCGCTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCGGCCGCCCCGGGAGCCG   2340
        P  A  L  N  H  A  V  L  R  A  L  M  H  A  A  A  P  G  A  A
2341  CCGACCTGCCCTGCTGCGTGCCCGCGCGCCTGTCGCCCATCTCCGTGCTCTTCTTTGACA   2400
        D  L  P  C  C  V  P  A  R  L  S  P  I  S  V  L  F  F  D  N
2401  ACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGTGCGGCTGCC   2460
        S  D  N  V  V  L  R  Q  Y  E  D  M  V  V  D  E  C  G  C  R
2461  GCTAACCCGGGGCGGGCAGGGACGCGGGCCCAACAATAAATGCCGCGTGG  2510
```

Fig 11B

human

~~07 614452~~
08/890002

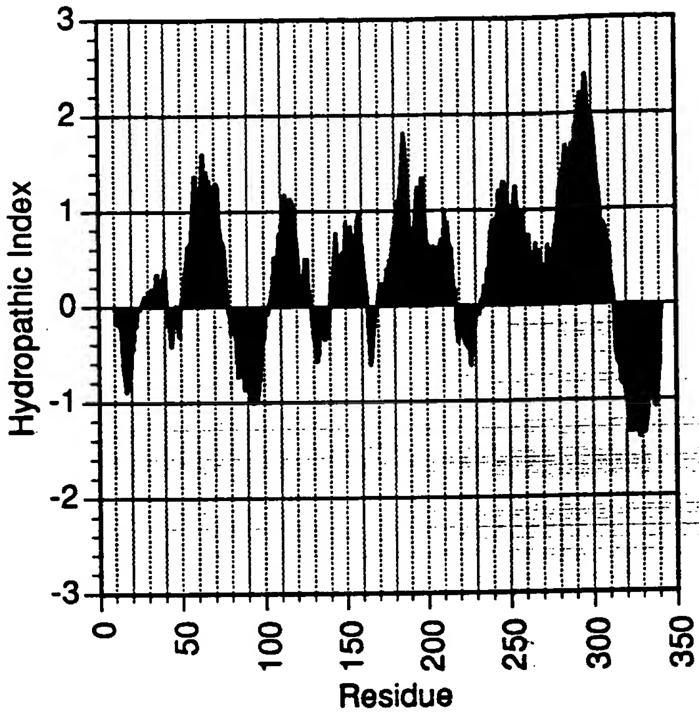

Fig 12

```
        1                                                            57
mGDF-1  MLPVCHRFCDH--LLLL-LLLPSTTLAPAPASMGPAAALLQVLGLPEAPRSVPTHRPVPP
hGDF-1  MPPPQQGPCGHHLLLLLALLLPSLPLTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPP
        1                                                            60

        58                                                           110
mGDF-1  VMWRLFRRRDPQEARVG-R---P---LRPCHVEELGVAGNIVRHIPDSGLSSRPAQPART
hGDF-1  VMWRLFRRRDPQETRSGSRRTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPVSA
        61                                                           120

        111                                 S                        166
mGDF-1  SGLCPEWTVVFDLSNVEPTERPTRARLELRLEAECEDT--GGWELSVALWAD-AE-HPGP
hGDF-1  AGHCPEWTVVFDLSAVEPAERPSRARLELRFAAAAAAAPEGGWELSVAQAGQGAGADPGP
        121                                                          180

        167                                                          225
mGDF-1  ELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAEASLLLVTL
hGDF-1  VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASLLLVTL
        181                                                          240

        226                                                          284
mGDF-1  DPRLC-PLPRLRRHTEPRVEVGPVGTCRTRRLHVSFREVGWHRWVIAPRGFLANFCQGTC
hGDF-1  DPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQC
        241                                                          300

        285                                                          344
mGDF-1  ALPETLRGPGGPPALNHAVLRALMHAAAPTPGAGSPCCVPERLSPISVLFFDNSDNVVLR
hGDF-1  ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCCVPARLSPISVLFFDNSDNVVLR
        301                                                          359

        345         357
mGDF-1  HYEDMVVDECGCR
hGDF-1  QYEDMVVDECGCR
        360         372
```

Fig 8a

```
        1                                                          60
mUOG-1  MAAAAATPRLEAPEPMPSYAQMLQRSWASALAAAQGCGDCGWGLARRGLAEHAHLAAPEL
hUOG-1  MAAAGPAAGPTGPEPMPSYAQLVQRGWGSALAAARGCTDCGWGLARRGLAEHAHLAPPEL
        1                                                          60

        61                                                        120
mUOG-1  LLAVLCALGWTALRWAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLACWSYCAYLL
hUOG-1  LLLALGALGWTALRSAATARLFRPLAKRCCLQPRDAAKMPESAWKFLFYLGSWSYSAYLL
        61                                                        120

        121                                                       180
mUOG-1  LGTSYPFFHDPPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVML
hUOG-1  FGTDYPFFHDPPSVFYDWTPGMAVPRDIAAAYLLQGSFYGHSIYATLYMDTWRKDSVVML
        121                                                       180

        181                                                       240
mUOG-1  VHHVVTLLLIASSYAFRYHNVGLLVFFLHDVSDVQLEFTKLNIYFKARGGAYHRLHGLVA
hUOG-1  LHHVVTLILIVSSYAFRYHNVGILVLFLHDISDVQLEFTKLNIYFKSRGGSYHRLHALAA
        181                                                       240

        241                                                       300
mUOG-1  NLGCLSFCFCWFWFRLYWFPLKVLYATCHCSLQSVPDIPYYFFFNILLLLLMVMNIYWFL
hUOG-1  DLGCLSFGFSWFWFRLYWFPLKVLYATSHCSLRTVPDIPFYFFFNALLLLLTLMNLYWFL
        241                                                       300

        301                                              350
mUOG-1  YIVAFAAKVLTGQMRELEDLREYDTLEAQTAKPCKAEKPLRNGLVKDKLF
hUOG-1  YIVAFAAKVLTGQVHELKDLREYDTAEAQSLKPSKAEKPLRNGLVKDKRF
        301                                              350
```

Fig 13b

~~614452~~

P.26/26

08/09 0002

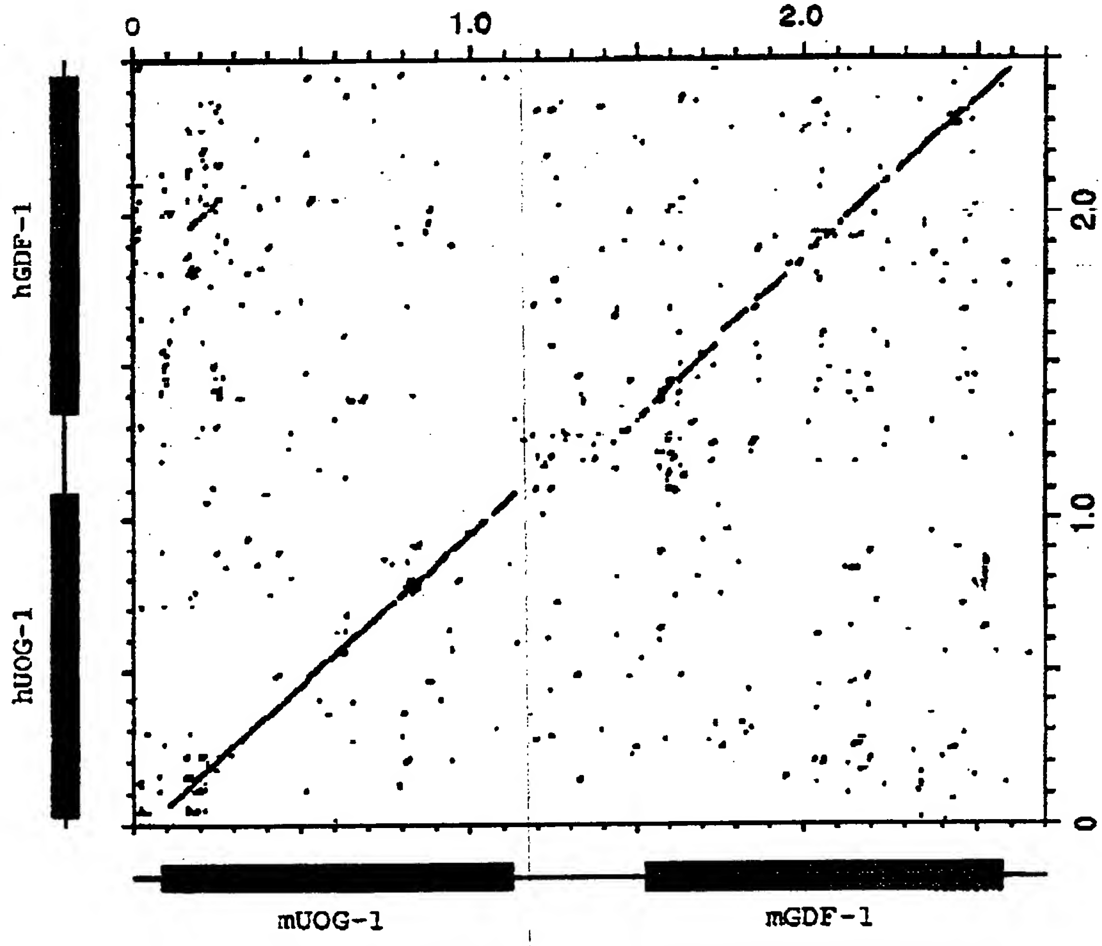

Fig 13c

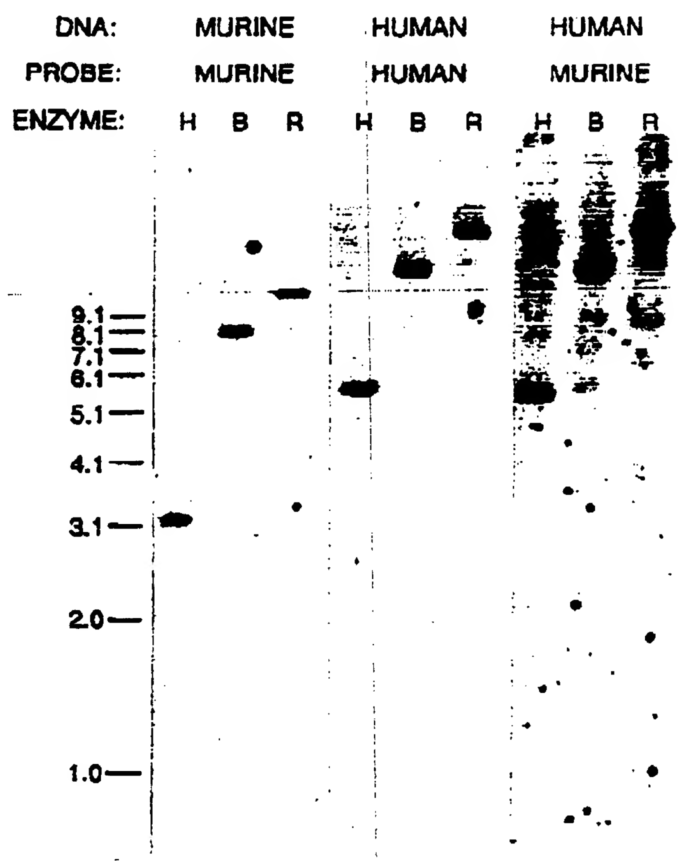
DNA: MURINE HUMAN HUMAN
PROBE: MURINE HUMAN MURINE
ENZYME: H B R H B R H B R
9.1
8.1
7.1
6.1
5.1
4.1
3.1
2.0
1.0

Fig 14